Amendments to the Claims

Please amend claims 1-6 and 16-23 so as to read as follows:

1.   A   method   of   three-dimensional   modeling   of   a bactericidal/permeability-increasing ("BPI") protein having antimicrobial, lipopolysaccharide-binding, and heparin-binding activities, the method comprising the step of using atomic coordinates of bactericidal/permeability-increasing ("BPI") protein, or fragment, analog or variant thereof, to model the BPI protein.

2.   A   method   of   three-dimensional   modeling   of   a bactericidal/permeability-increasing ("BPI") related lipid transfer protein having antimicrobial,   lipopolysaccharide-binding,   and   heparin-binding   activities,   the method   comprising   the   step   of   using   atomic   coordinates   of bactericidal/permeability-increasing ("BPI") protein, or fragment, analog or variant thereof, to model the BPI-related lipid transfer protein.

3.   The method according to claim 2, wherein the BPI-related lipid transfer protein is lipopolysaccharide-binding protein (LBP), cholesteryl ester transferase protein (CETP) or phospholipid transfer protein (PLTP), or fragment, analog or variant thereof.

4.   The method according to any of claims 1-3, wherein the BPI protein comprises a binding site characterized by amino acid residues of at least one binding pocket as defined in Table 3.

5.   The method according to any of claims 1-3, wherein the BPI protein comprises a binding site characterized by at least one amino acid sequence, or variant of the sequence, selected from positions about 17 to about 45, positions about 36 to about 54, positions about 65 to about 99, positions about 84 to about 109, positions about 142 to about 164, or positions about 142 to about 169 of BPI of SEQ ID NO: 2.

6.   The method according to any of claims 1-3, wherein the BPI protein comprises a binding site characterized by amino acid residues of at least one binding pocket as defined in Table 3 and a binding site characterized by at least one amino acid sequence, or variant of the sequence, selected from positions about 17 to about 45, positions about 36 to about 54, positions about 65 to about 99, positions about 84

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to about 109, positions about 142 to about 164, or positions about 142 to about 169 of BPI of SEQ ID NO: 2.

15. The method according to any of claims 1 – 3, wherein said atomic coordinates are according to Table 4.

16. A method of three-dimensional modeling of a bactericidal/permeability-increasing ("BPI") protein having antimicrobial, lipopolysaccharide-binding, and heparin-binding activities, the method comprising the steps of:

(a) providing three-dimensional atomic coordinates derived from X-ray diffraction measurements of a BPI protein in a computer readable format;

(b) inputting the data from step (a) into a computer with appropriate software programs;

(c) generating a three-dimensional structural representation of the BPI protein suitable for visualization and further computational manipulation.

17. A method of three-dimensional modeling of a bactericidal/permeability-increasing ("BPI")-related lipid transfer protein having antimicrobial, lipopolysaccharide-binding, and heparin-binding activities, the method comprising the steps of:

(a) providing three-dimensional atomic coordinates derived from X-ray diffraction measurements of a BPI protein in a computer readable format;

(b) inputting the data from step (a) into a computer with appropriate software programs;

(c) generating a three-dimensional structural representation of the BPI-related lipid transfer protein suitable for visualization and further computational manipulation.

18. The method according to any of claims 16-17, wherein the BPI protein comprises a binding site characterized by amino acid residues of at least one binding pocket as defined in Table 3.

19. The method according to any of claims 16-17, wherein the BPI protein comprises a binding site characterized by at least one amino acid sequence,

or variant of the sequence, selected from positions about 17 to about 45, positions about 36 to about 54, positions about 65 to about 99, positions about 84 to about 109, positions about 142 to about 164, or positions about 142 to about 169 of BPI of SEQ ID NO: 2.

20. The method according to any of claims 16-17, wherein the BPI protein comprises a binding site characterized by amino acid residues of at least one binding pocket as defined in Table 3 and a binding site characterized by at least one amino acid sequence, or variant of the sequence, selected from positions about 17 to about 45, positions about 36 to about 54, positions about 65 to about 99, positions about 84 to about 109, positions about 142 to about 164, or positions about 142 to about 169 of BPI of SEQ ID NO: 2.

21. A method for providing an atomic model of a BPI protein, or fragment, analog or variant thereof, having antimicrobial, lipopolysaccharide-binding, and heparin-binding activities, the method comprising

    (a) providing a computer readable medium having stored thereon atomic coordinate/x-ray diffraction data of the BPI protein, or fragment, analog or variant thereof, in crystalline form, the data sufficient to model the three-dimensional structure of the BPI protein, or fragment, analog or variant thereof;

    (b) analyzing, on a computer using at least one subroutine executed in said computer, atomic coordinate/x-ray diffraction data from (a) to provide atomic coordinate data output defining an atomic model of said BPI protein, or fragment, analog or variant thereof, said analyzing utilizing at least one computing algorithm selected from the group consisting of data processing and reduction, auto-indexing, intensity scaling, intensity merging, amplitude conversion, truncation, molecular replacement, molecular alignment, molecular refinement, electron density map calculation, electron density modification, electron map visualization, model building, rigid body refinement, positional refinement; and

    (c) obtaining atomic coordinate data defining the three-dimensional structure of at least one of said BPI protein, or fragment, analog or variant thereof.

22. A method according to claim 21, wherein said computer readable medium further has stored thereon data corresponding to a nucleic acid sequence or

an amino acid sequence data comprising at least one structural domain or functional domain of a BPI, LBP, CETP or PLTP corresponding to at least one BPI or mutant primary sequence of Figures 2-20 or Table 2, or a fragment thereof; and wherein said analyzing step further comprises analyzing said sequence data.

23.   A computer-based system for providing atomic model data of the three-dimensional structure of BPI protein, or fragment, analog or variant thereof, a BPI mutant or a BPI fragment, having antimicrobial, lipopolysaccharide-binding, and heparin-binding activities, the system comprising the following elements:

(a)   at least one computer readable medium (CRM) having stored thereon atomic coordinate/x-ray diffraction data of said BPI protein, or fragment, analog or variant thereof;

(b)   at least one computing subroutine that, when executed in a computer, causes the computer to analyze atomic coordinate/x-ray diffraction data from (a) to provide atomic coordinate data output defining an atomic model of said BPI protein, or fragment, analog or variant thereof, said analyzing utilizing at least one computing subroutine selected from the group consisting of data processing and reduction, auto-indexing, intensity scaling, intensity merging, amplitude conversion, truncation, molecular replacement, molecular alignment, molecular refinement, electron density map calculation, electron density modification, electron map visualization, model building, rigid body refinement, positional refinement; and

(c)   retrieval means for obtaining atomic coordinate output data substantially defining the three-dimensional structure of said BPI protein, or fragment, analog or variant thereof.

REMARKS

Claims 1-25 are pending in this application. Claims 1-6 and 16-23 were considered and rejected under 35 U.S.C. §§ 101 and 112 in the Office Action of April 24, 2001. Claim 15 was not considered on the merits because it was the subject of an objection as being in improper form for a multiple dependent claim. Claims 7-14 and 24-25 were withdrawn from consideration in response to Applicants' election of Specie A (claims 1-6 and 15-23). A copy